

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
(B) STREET: Four Embarcadero Center, Suite 1100
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/878,474
(B) FILING DATE: 18-JUN-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/020,150
(B) FILING DATE: 20-JUN-1996
-
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Siebert, J. Suzanne
(B) REGISTRATION NUMBER: 28,758
(C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/248-5500
(B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Leu Asn Val Leu Arg Ile Cys Ile Ile Val Cys Leu Val Asn
1 5 10 15

Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
20 25 30

Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
35 40 45

Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
50 55 60

Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
65 70 75 80

Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
85 90 95

Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
100 105 110

Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
115 120 125

Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
130 135 140

Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
145 150 155 160

Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
165 170 175

Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
180 185 190

Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
195 200 205

Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
210 215 220

Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
225 230 235 240

Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
245 250 255

Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
260 265 270

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT 60
AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT 120
GATGGAGCAG GAAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC 180
AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT 240
AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAAC TATTT 300
GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC 360
TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG 420
AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTACTGA AAAGCCTGGT 480
GCCAAGATGT TCTGGAACAA TTTTTTGGTT AAAATGAATG GAGCCCCACA GAATACAAGC 540
CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG 600
AATATTGTAC ATGAAAAC TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA 660
TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG 720
CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA 780
AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTTCCACCAA 840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
 TACAGTATGG AAATGCCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
 ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
 AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCATCA GTTGCAAGAT AAAAGGCAAT 1080
 ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
 AACTGTAA GGGGTAATGT AATAATAGGG ACTAACAACC AATCAGCAGG TATGATTTAC 1200
 TGGTCACCTG TTTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTTACTGC TTCTGGGCAA 1260
 AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTACTGA ATTAATTGTA TTTATTTTCA 1320
 TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACCTTTA TTAATGTACA ATAAATGTTC 1380
 TTGTTTCTTT AAAAAAAAAA AAAAAGCTCGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Arg Thr Arg Lys Val Asp Ser Leu Leu Leu Leu Ala Ile Pro
 1 5 10 15
 Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
 20 25 30
 Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
 35 40 45
 Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
 50 55 60
 Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
 65 70 75 80
 Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
 85 90 95

Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
 100 105 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
 115 120 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
 130 135 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145 150 155 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
 165 170 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
 195 200 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
 290 295 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTTGGTT 60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT 120
CTAATTCTGC ACTTTTAAAT TATCTGAGTA ATTGTTTATT TTGTATTGGA TGGGACTAAA 180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG 240
TTGCTTTTAC ATGTGCCAG ATTTTCCCTG TATTCCTGT ATTCCCTCTA AAGTAAGCCT 300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC 360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG 420
AGCCTGTGCG GATCCCCATG TSCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCAACC 480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC 540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCCATTT 600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA 660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT 720
GTGAAGAGCT GCCCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG 780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG 840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCAAAAG ACGTATCTCA 900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG 960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCTTA 1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTGTG CCCCAGCTT GTTGCCAATG 1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGGAAG 1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA 1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATTCCCAAC AAAACAGCA 1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAAACTCT ATGGACTTTG 1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT 1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT 1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG 1500
 CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC 1560
 AAGTGTTTGA TACTTGGGGA AAGTGAAC TAATGCAATGG TAAATCAGAG AAAAGTTGAC 1620
 CAATGTTGCT TTTCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT 1680
 CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT 1740
 ATTTTATCAT AAATGAAGAG CTGGTTTAGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC 1800
 CTACTTTGTC AATTCTGTTT TAAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA 1860
 AAAAAAAAAA AAAAA 1875

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
 1 5 10 15
 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu
 20 25 30
 Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
 35 40 45
 Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
 50 55 60
 Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
 65 70 75 80
 Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
 85 90 95
 Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
 100 105 110

Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
 115 120 125
 Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
 130 135 140
 Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
 145 150 155 160
 Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
 165 170 175
 Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
 180 185 190
 Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
 195 200 205
 Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val
 210 215 220
 Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
 225 230 235 240
 Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
 245 250 255
 Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
 260 265 270
 Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
 275 280 285
 Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
 290 295 300
 Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
 305 310 315 320
 Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
 325 330 335
 Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
 340 345 350
 Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
 355 360 365
 Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
 370 375 380

Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
 385 390 395 400
 Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
 405 410 415
 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
 420 425 430
 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
 435 440 445
 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
 450 455 460
 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
 465 470 475 480
 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
 485 490 495
 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
 500 505 510
 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
 515 520 525
 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
 530 535 540
 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
 545 550 555 560
 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
 565 570 575
 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
 580 585 590
 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
 595 600 605
 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
 610 615 620
 Ser Gly Glu Val Phe Leu Lys Lys Gln Leu Asn Ser Asp His Ser Glu
 625 630 635 640
 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
 645 650 655

Ser Thr Asn Ala Thr Val Lys Phe Ile Leu Thr Asp Ser Phe Pro Ser
 660 665 670
 Asn Val Glu Val Val Ile Leu Gln Pro Ser Ala Glu Glu Gln His Gln
 675 680 685
 Ile Asp Met Ser Ile Ile Phe Ile Ala Val Leu Ala Gly Gly Cys Ala
 690 695 700
 Leu Leu Leu Leu Ala Ile Phe Phe Val Ala Cys Thr Cys Lys Lys Lys
 705 710 715 720
 Ala Gly Glu Phe Lys Gln Val Pro Glu Gln His Gly Thr Cys Asn Glu
 725 730 735
 Glu Arg Leu Leu Ser Thr Pro Ser Pro Gln Ser Val Ser Ser Ser Leu
 740 745 750
 Ser Gln Ser Glu Ser Cys Gln Leu Ser Ile Asn Thr Glu Ser Glu Asn
 755 760 765
 Cys Ser Val Ser Ser Asn Gln Glu Gln His Gln Gln Thr Gly Ile Lys
 770 775 780
 His Ser Ile Ser Val Pro Ser Tyr His Thr Ser Gly Trp His Leu Asp
 785 790 795 800
 Asn Cys Ala Met Ser Ile Ser Gly His Ser His Met Gly His Ile Ser
 805 810 815
 Thr Lys Asp Ser Gly Lys Gly Asp Ser Asp Phe Asn Asp Ser Asp Ser
 820 825 830
 Asp Thr Ser Gly Glu Ser Gln Lys Lys Ser Ile Glu Gln Pro Met Gln
 835 840 845
 Ala Gln Ala Ser Ala Gln Tyr Thr Asp Glu Ser Ala Gly Phe Arg His
 850 855 860
 Ala Asp Asn Tyr Phe Ser His Arg Ile Asn Lys Gly Pro Glu Asn Gly
 865 870 875 880
 Asn Cys Thr Leu Gln Tyr Glu Lys Gly Tyr Arg Leu Ser Tyr Ser Val
 885 890 895
 Ala Pro Ala His Tyr Asn Thr Tyr His Ala Arg Met Pro Asn Leu His
 900 905 910
 Ile Pro Asn His Thr Leu Arg Asp Pro Tyr Tyr His Ile Asn Asn Pro
 915 920 925

Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 930 935 940
 Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 945 950 955 960
 Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 965 970 975
 Thr Thr Phe

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTC~~CC~~CAG AGATGAACTC CTTGAGATTG TTTTAAATGA CTGCAGGTCT GGAAGGATTC 60
 ACATTGCCAC ACTGTTTCTA GGCATGAAAA AACTGCAAGT TTCAACTTTG TTTTGGGTGC 120
 AACTTTGATT CTTCAAGATG CTGCTTCTCT TCAGAGCCAT TCCAATGCTG CTGTTGGGAC 180
 TGATGGTTTT ACAAAACAGAC TGTGAAATTG CCCAGTACTA CATAGATGAA GAAGAACCCC 240
~~GTGGCACTGT AATTGCAGTG TTGTCACAAC ACTCCATATT TAACACTACA GATATACCTG 300~~
 CAACCAATTT CCGTCTAATG AAGCAATTTA ATAATTCCTT TATCGGAGTC CGTGAGAGTG 360
 ATGGGCAGCT GAGCATCATG GAGAGGATTG ACCGGGAGCA AATCTGCAGG CAGTCCCTTC 420
 ACTGCAACCT GGCTTTGGAT GTGGTCAGCT TTTCCAAAGG ACACTTCAAG CTTCTGAACG 480
 TGAAAGTGA GGTGAGAGAC ATTAATGACC ATAGCCCTCA CTTTCCCAGT GAAATAATGC 540
 ATGTGGAGGT GTCTGAAAGT TCCTCTGTGG GCACCAGGAT TCCTTTAGAA ATTGCAATAG 600
 ATGAAGATGT TGGGTCCAAC TCCATCCAGA ACTTTCAGAT CTCAAATAAT AGCCACTTCA 660
 GCATTGATGT GCTAACCAGA GCAGATGGGG TGAAATATGC AGATTTAGTC TTAATGAGAG 720
 AACTGGACAG GGAAATCCAG CCAACATACA TAATGGAGCT ACTAGCAATG GATGGGGGTG 780

TACCATCACT	ATCTGGTACT	GCAGTGGTTA	ACATCCGAGT	CCTGGACTTT	AATGATAACA	840
GCCCAGTGTT	TGAGAGAAGC	ACCATTGCTG	TGGACCTAGT	AGAGGATGCT	CCTCTGGGAT	900
ACCTTTTGTT	GGAGTTACAT	GCTACTGACG	ATGATGAAGG	AGTGAATGGA	GAAATTGTTT	960
ATGGATTGAG	CACTTTGGCA	TCTCAAGAGG	TACGTCAGCT	ATTTAAAATT	AACTCCAGAA	1020
CTGGCAGTGT	TACTCTTGAA	GGCCAAGTTG	ATTTTGAGAC	CAAGCAGACT	TACGAATTTG	1080
AGGTACAAGC	CCAAGATTTG	GGCCCCAACC	CACTGACTGC	TACTTGTAAG	GTAAGTGTTC	1140
ATATACTTGA	TGTAAATGAT	AATACCCCAG	CCATCACTAT	TACCCCTCTG	ACTACTGTAA	1200
ATGCAGGAGT	TGCCTATATT	CCAGAAACAG	CCACAAAGGA	GAACCTTTATA	GCTCTGATCA	1260
GCACTACTGA	CAGAGCCTCT	GGATCTAATG	GACAAGTTCG	CTGTACTCTT	TATGGACATG	1320
AGCACTTTAA	ACTACAGCAA	GCTTATGAGG	ACAGTTACAT	GATAGTTACC	ACCTCTACTT	1380
TAGACAGGGA	AAACATAGCA	GCGTACTCTT	TGACAGTAGT	TGCAGAAGAC	CTTGGCTTCC	1440
CCTCATTGAA	GACCAAAAAG	TACTACACAG	TCAAGGTTAG	TGATGAGAAT	GACAATGCAC	1500
CTGTATTTTC	TAAACCCCAG	TATGAAGCTT	CTATTCTGGA	AAATAATGCT	CCAGGCTCTT	1560
ATATAACTAC	AGTGATAGCC	AGAGACTCTG	ATAGTGATCA	AAATGGCAAA	GTAAATTACA	1620
GAAGTGTGGA	TGCAAAAGTG	ATGGGTCAGT	CACTAACAAC	ATTTGTTTCT	CTTGATGCGG	1680
ACTCTGGAGT	ATTGAGAGCT	GTTAGGTCTT	TAGACTATGA	AAAACCTTAA	CAACTGGATT	1740
TTGAAATTGA	AGCTGCAGAC	AATGGGATCC	CTCAACTCTC	CACTCGCGTT	CAACTAAATC	1800
TCAGAAATAGT	TGATCAAAAT	GATAATTGCC	CTGTGATAAC	TAATCCTCTT	CTTAATAATG	1860
GCTCGGGTGA	AGTTCTGCTT	CCCATCAGCG	CTCCTCAAAA	CTATTTAGTT	TTCCAGCTCA	1920
AAGCCGAGGA	TTCAGATGAA	GGGCACAACT	CCCAGCTGTT	CTATACCATA	CTGAGAGATC	1980
CAAGCAGATT	GTTTGCCATT	AACAAAGAAA	GTGGTGAAGT	GTTCCCTGAA	AAACAATTAA	2040
ACTCTGACCA	TTCAGAGGAC	TTGAGCATAG	TAGTTGCAGT	GTATGACTTG	GGAAGACCTT	2100
CATTATCCAC	CAATGCTACA	GTAAATTCA	TCCTCACCGA	CTCTTTTCCT	TCTAACGTTG	2160
AAGTCGTTAT	TTTGCAACCA	TCTGCAGAAG	AGCAGCACCA	GATCGATATG	TCCATTATAT	2220
TCATTGCAGT	GCTGGCTGGT	GGTTGTGCTT	TGCTACTTTT	GGCCATCTTT	TTTGTGGCCT	2280
GTACTTGTA	AAAGAAAGCT	GGTGAATTTA	AGCAGGTACC	TGAACAACAT	GGAACATGCA	2340

ATGAAGAACG	CCTGTTAAGC	ACCCCATCTC	CCCAGTCGGT	CTCTTCTTCT	TTGTCTCAGT	2400
CTGAGTCATG	CCAACCTCTC	ATCAATACTG	AATCTGAGAA	TTGCAGCGTG	TCCTCTAACC	2460
AAGAGCAGCA	TCAGCAAACA	GGCATAAAGC	ACTCCATCTC	TGTACCATCT	TATCACACAT	2520
CTGGTTGGCA	CCTGGACAAT	TGTGCAATGA	GCATAAGTGG	ACATTCTCAC	ATGGGGCACA	2580
TTAGTACAAA	GGACAGTGGC	AAAGGAGATA	GTGACTTCAA	TGACAGTGAC	TCTGATACTA	2640
GTGGAGAATC	ACAAAAGAAG	AGCATTGAGC	AGCCAATGCA	GGCACAAGCC	AGTGCTCAAT	2700
ACACAGATGA	ATCAGCAGGG	TTCCGACATG	CCGATAACTA	TTTCAGCCAC	CGAATCAACA	2760
AGGGTCCAGA	AAATGGGAAC	TGCACATTGC	AATATGAAAA	GGGCTATAGA	CTGTCTTACT	2820
CTGTAGCTCC	TGCTCATTAC	AATACCTACC	ATGCAAGAAT	GCCTAACCTG	CACATACCGA	2880
ACCATACCCT	TAGAGACCTT	TATTACCATA	TCAATAATCC	TGTTGCTAAT	CGGATGCACG	2940
CGGAATATGA	AAGAGATTTA	GTCAACAGAA	GTGCAACGTT	ATCTCCGCAG	AGATCGTCTA	3000
GCAGATACCA	AGAATTCAAT	TACAGTCCGC	AGATATCAAG	ACAGCTTCAT	CCTTCAGAAA	3060
TTGCTACAAC	CTTTTAATCA	TTAGGCATGC	AAGTGAGAAT	GCACAAAGGC	AAGTGCTTTA	3120
GCATGAAAGC	TAAATATATG	GAGTCTCCCC	TTTCCCTCTG	ATGGATGGGG	GGAGACACAG	3180
GACAGTGCAT	AAATATACAG	CTGCTTTCTA	TTTGCATTTC	ACTTGGAAT	TTTTTGTTTT	3240
TTTACATAT	TTATTTTCC	TGAATTGAAT	GTGACATTGT	CCTGTCACCT	AACTAGCAAT	3300
TAAATCCACA	GACCTACAGT	CAAATATTG	AGGGCCCCTG	AAACAGCACA	TCAGTCAGGA	3360
CCTAAAGTGG	CCTTTTTACT	TTAGCAGCT	CCTGGGTCTG	CCCTCTGTGT	TAATCAGCCC	3420
CTGGTCAAGT	CCTGAGTAGG	ATCATGGCGT	TTTTATATGC	ATCTCACCTA	CTTTGGACGT	3480
GATTTACACA	TAATAGGAAA	CGCTTGSTTT	CAGTGAAGTC	TGTGTTGTAT	ATATTCTGTT	3540
ATATACACGC	ATTTTGTGTT	TGTGTATATA	TTTCAAGTCC	ATTCAGATAT	GTGTATATAG	3600
TGCAGACCTT	GTAAATTAAA	TATTCTGATA	CTTTTTCCTC	AATAAATATT	TAAAT	3655

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Cys Cys Gly Pro Gly Arg Met Leu Leu Gly Trp Ala Gly Leu
1 5 10 15
Leu Val Leu Ala Ala Leu Cys Leu Leu Gln Val Pro Gly Ala Gln Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
 290 295 300
 Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
 305 310 315 320
 Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG 60
 CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCCGAG CTCAGGCTGC AGCCTGTGAG 120
 CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC 180
 CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG 240
 GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC 300
 ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA 360
 CAGGGCTGCG AGCCCATTTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC 420
 GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG 480
 GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA 540
 CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC 600

TATGTCATCC	GGGCTAAAGT	TAAAGAGGTA	AAGATGAAAT	GTCATGATGT	GACCGCCGTT	660
GTGGAAGTGA	AGGAAATTCT	AAAGGCATCA	CTGGTAAACA	TTCCAAGGGA	CACCGTCAAT	720
CTTTATACCA	CCTCTGGCTG	CCTCTGTCCT	CCACTTACTG	TCAATGAGGA	ATATGTCATC	780
ATGGGCTATG	AAGACGAGGA	ACGTTCCAGG	TTACTCTTGG	TAGAAGGCTC	TATAGCTGAG	840
AAGTGGAAGG	ATCGGCTTGG	TAAGAAAGTC	AAGCGCTGGG	ATATGAAACT	CCGACACCTT	900
GGACTGGGTA	AAACTGATGC	TAGCGATTCC	ACTCAGAATC	AGAAGTCTGG	CAGGAACTCT	960
AATCCCCGGC	CAGCACGAG	CTAAATCCTG	AAATGTAAAA	GGCCACACCC	ACGGACTCCC	1020
TTCTAAGACT	GGCGCTGGTG	GACTAACAAA	GGAAAACCGC	ACAGTTGTGC	TCGTGACCGA	1080
TTGTTTACCG	CAGACACCGC	GTGGCTACCG	AAGTTACTTC	CGGTCCCCTT	TCTCCTGCTT	1140
CTTAATGGCG	TGGGGTTAGA	TCCTTTAATA	TGTTATATAT	TCTGTTTCAT	CAATCACGTG	1200
GGGACTGTTC	TTTTGCAACC	AGAATAGTAA	ATTAAATATG	TTGATGCTAA	GGTTTCTGTA	1260
CTGGACTCCC	TGGGTTTAAT	TTGGTGTTC	GTACCCTGAT	TGAGAATGCA	ATGTTTCATG	1320
TAAAGAGAGA	ATCCTGGTCA	TATCTCAAGA	ACTAGATATT	GCTGTAAGAC	AGCCTCTGCT	1380
GCTGCGCTTA	TAGTCTTG	TTGTATGCC	TTTGTCCATT	TCCCTCATGC	TGTGAAAGTT	1440
ATACATGTTT	ATAAAGGTAG	AACGGCATT	TGAAATCAGA	CACTGCACAA	GCAGAGTAGC	1500
CCAACACCAG	GAAGCATTTA	TGAGGAAACG	CCACACAGCA	TGACTTATTT	TCAAGATTGG	1560
CAGGCAGCAA	AATAAATAGT	GTTGGGAGCC	AAGAAAAGAA	TATTTTGCCT	GGTTAAGGGG	1620
CACACTGGAA	TCAGTAGCCC	TTGAGCCATT	AACAGCAGTG	TTCTTCTGGC	AAGTTTTTGA	1680
TTTGTTTATA	AATGTATTCA	CGAGCATTAG	AGATGAACTT	ATAACTAGAC	ATCTGTTGTT	1740
ATCTCTATAG	CTCTGCTTCC	TTCTAAATCA	AACCCATTGT	TGGATGCTCC	CTCTCCATTC	1800
ATAAATAAAT	TTGGCTTGCT	GTATTGGCCA	GGAAAAGAAA	GTATTAAAGT	ATGCATGCAT	1860
GTGCACCAGG	GTGTTATTTA	ACAGAGGTAT	GTAACCTCTAT	AAAAGACTAT	AATTTACAGG	1920
ACACGGAAAT	GTGCACATTT	GTTTACTTTT	TTTCTTCCTT	TTGCTTTGGG	CTTGTGATTT	1980
TGGTTTTTGG	TGTGTTTATG	TCTGTATTTT	GGGGGGTGGG	TAGGTTTAAG	CCATTGCACA	2040
TTCAAGTTGA	ACTAGATTAG	AGTAGACTAG	GCTCATTGGC	CTAGACATTA	TGATTTGAAT	2100

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
1 5 10 15
Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
165 170 175

Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
 195 200 205
 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
 290 295 300
 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
 305 310 315 320
 Arg Gln Ala Arg Asn
 325

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1893 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGGAGCGG GCCTTTTGGC GTCCACTGCG CGGCTGACCC CTGCCCCATC TGCCGGGATC 60
 ATGGTCTGCG GCAGCCCGGG AGGGATGCTG CTGCTGCGGG CCGGGCTGCT TGCCCTGGCT 120
 GCTCTCTGCC TGCTCCGGGT GCCCGGGGCT CGGGCTGCAG CCTGTGAGCC CGTCCGCATC 180
 CCCCTGTGCA AGTCCCTGCC CTGGAACATG ACTAAGATGC CCAACCACCT GCACCACAGC 240

ACTCAGGCCA	ACGCCATCCT	GGCCATCGAG	CAGTTCGAAG	GTCTGCTGGG	CACCCACTGC	300
AGCCCCGATC	TGCTCTTCTT	CCTCTGTGCC	ATGTACGCGC	CCATCTGCAC	CATTGACTTC	360
CAGCACGAGC	CCATCAAGCC	CTGTAAGTCT	GTGTGCGAGC	GGGCCCCGCA	GGGCTGTGAG	420
CCCATACTCA	TCAAGTACCG	CCACTCGTGG	CCGGAGAACC	TGGCCTGCGA	GGAGCTGCCA	480
GTGTACGACA	GGGGCGTGTG	CATCTCTCCC	GAGGCCATCG	TTACTGCGGA	CGGAGCTGAT	540
TTTCCTATGG	ATTCTAGTAA	CGGAACTGT	AGAGGGGCAA	GCAGTGAACG	CTGTAAATGT	600
AAGCCTATTA	GAGCTACACA	GAAGACCTAT	TTCCGGAACA	ATTACAATA	TGTCATTCCG	660
GCTAAAGTTA	AAGAGATAAA	GACTAAGTGC	CATGATGTGA	CTGCAGTAGT	GGAGGTGAAG	720
GAGATTCTAA	AGTCCTCTCT	GGTAAACATT	CCACGGGACA	CTGTCAACCT	CTATACCAGC	780
TCTGGCTGCC	TCTGCCCTCC	ACTTAATGTT	AATGAGGAAT	ATATCATCAT	GGGCTATGAA	840
GATGAGGAAC	GTTCCAGATT	ACTCTTGGTG	GAAGGCTCTA	TAGCTGAGAA	GTGGAAGGAT	900
CGACTCGGTA	AAAAAGTTAA	GCGCTGGGAT	ATGAAGCTTC	GTCATCTTGG	ACTCAGTAAA	960
AGTGATTCTA	GCAATAGTGA	TTCCACTCAG	AGTCAGAAGT	CTGGCAGGAA	CTCGAACCCC	1020
CGGCAAGCAC	GCAACTAAAT	CCCGAAATAC	AAAAAGTAAC	ACAGTGGACT	TCCTATTAAG	1080
ACTTACTTGC	ATTGCTGGAC	TAGCAAAGGA	AAATTGCACT	ATTGCACATC	ATATTCTATT	1140
GTTTACTATA	AAAATCATGT	GATAACTGAT	TATTACTTCT	GTTTCTCTTT	TGGTTTCTGC	1200
TTCTCTCTTC	TCTCAACCCC	TTTGTAAATGG	TTTGGGGGCA	GACTCTTAAG	TATATTGTGA	1260
GTTTCTTATT	TCACTAATCA	TGAGAAAAAC	TCTTCTTTTG	CAATAATAAT	AAATTAAACA	1320
TGCTGTTACC	AGAGCCTCTT	TGCTGAGTCT	CCAGATGTTA	ATTTACTTTC	TGCACCCCAA	1380
TTGGGAATGC	AATATTGGAT	GAAAAGAGAG	GTTTCTGGTA	TTCACAGAAA	GCTAGATATG	1440
CCTTAAAACA	TACTCTGCCG	ATCTAATTAC	AGCCTTATTT	TTGTATGCCT	TTTGGGCATT	1500
CTCCTCATGC	TTAGAAAGTT	CCAAATGTTT	ATAAAGGTAA	AATGGCAGTT	TGAAGTCAAA	1560
TGTCACATAG	GCAAAGCAAT	CAAGCACCAG	GAAGTGTTTA	TGAGGAAACA	ACACCCAAGA	1620
TGAATTATTT	TTGAGACTGT	CAGGAAGTAA	AATAAATAGG	AGCTTAAGAA	AGAACATTTT	1680
GCCTGATTGA	GAAGCACAAC	TGAAACCAGT	AGCCGCTGGG	GTGTTAATGG	TAGCATTCTT	1740
CTTTTGCCAA	TACATTTGAT	TTGTTTATGA	ATATATTAAT	CAGCATTAGA	GAAATGAATT	1800

ATAACTAGAC ATCTGCTGTT ATCACCATAG TTTTGTAA TTTGCTTCCT TTAAATAAA 1860

CSCATTGGTG AAAGTCAAAA AAAAAAAAAA AAA 1893

1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893